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1 ATTTTATTATTACCAATCTTATATAATAATATAATTTCTCTTACAAAAATCTCTAATG 60
61 TTTTATACCTAATATATATATCTGGCTTGATCTACTTTGCACTTCCACTATTGTTAAT 120
121 TTATTTCACTATTTTTAGGTGTAAT**TGA**ATTGCAAAAAATCTTATAACAACACTGCATT 180
M N C K K I L I T T A L
181 AATATCATTAATGTACTCTATTTCCAAAGCATAATCTTTTCTGATACTATACAAGATGGTAA 240
I S L M Y S I P S I S F S D T I Q D G N
241 CATGGGTGGTAACCTTCTATATATTAGTGGAAAGTATGTACCAAGTGTCTCACATTTTGGTAG 300
M G G N F Y I S G K Y V P S V S H F G S
301 CTTCCTCAGCTAAAGAAGAAAGCAAAATCAACTGTTGGAGTTTTTTGGATTAAACACATGATTG 360
F S A K E E S K S T V G V F G L K H D W
361 GGATGGAAGTCCAATACTTAAGAATAAACACGCTGACTTTACTGTGCCAAACTATTCGTT 420
D G S P I L K N K H A D F T V P N Y S F
421 CAGATACGAGAACAAATCCATTTTCTAGGGTTTGCAAGGAGCTATCGGTTACTCAATGGGTGG 480
R Y E N N P F L G F A G A I G Y S M G G
481 CCCAAGAAATAGAATTCGAAATATCTTATGAAGCATTCGACGTAAAAAGTCCTAATATCAA 540
P R I E F E I S Y E A F D V K S P N I N
541 TTATCAAAAATGACGCGCACAGGTACTGCGCTCTATCTCATCACACATCGGCAGCCCATGGA 600
Y Q N D A H R Y C A L S H H T S A A M E
601 AGCTGATAAATTTGTCTTCTTAAAAAACGAAGGGTTAATTGACATATCACTTGCAATAAA 660
A D K F V F L K N E G L I D I S L A I N
661 TGCATGTTATGATATAATAAATGACAAAAGTACCTGTTTCTCCTTATATATGCGCAGGTAT 720
A C Y D I I N D K V P V S P Y I C A G I

Fig. 1A

721 TGGTACTGATTTGATTTCTATGTTGAAGCTACAAGTCCTAAAATTTCTTACCAAGGAAA 780
G T D L I S M F E A T S P K I S Y Q G K
841 CAGGATCATAGGTAATGAGTTTAGAGATATTCCTGCAATAGTACCTAGTAACTCAACTAC 900
R I I G N E F R D I P A I V P S N S T T
901 AATAAGTGGACCAACAATTTGCAACAGTAACACTAAATGTGTGTCACTTTGGTTTAGAACT 960
I S G P Q F A T V T L N V C H F G L E L
961 TGGAGGAAGATTTAACTTCTAAATTTTATTGTTGCCACATATTAAAAATGATCTAAACTTG 1020
G G R F N F (SEQ. ID NO: 2)
1021 TTTTAAWTATTGCTACATACAAAAAAGAAAAATAGTGGCAAAAGAAATGTAGCAATAAGA 1080
1081 GGGGGGGGGACCAAAATTTATCTTCTATGCTTCCCAAGTTTTTTCYCGCTATTATGA 1140
1141 CTTAAACAACAGAAAGTAATATCCTCAGGAAAACTTATCTCAAAATATTTTATTATTA 1200
1201 CCAATCTTATATAATATAATTAATTTCTCTTACAAAAATCACTAGTATTTTATACCAAAA 1260
1261 TATATATTCTGACTTGCTTTTCTTCTGCACTTCTACTATTTTAAATTTTATTTGTCACTAT 1320
1321 TAGGTTATAATAAWATGAATTGCMAAAAGATTTTTCATAGCAAGTGCATTGATATCACTAA 1380
1381 TGTCCTTCTTACCTAGCGTATCTTTTCTGAATCAATACATGAAGATAAATAAATGGTA 1440
1441 ACTTTTACATTAGTGCAAAAGTATATGCCAAGTGCCCTCACACTTTGGCGTATTTTCAGTTA 1500
1501 AAGAAGAGAAAAACACAACAACTGGAGTTTTCGGATTAAACAAGATTGGGACGGAGCAA 1560
1561 CACTAAAGGATGCAAGCWGCAGCCACACAWTAGACCCCAAGTACAAATG 1607
(SEQ ID NO: 1)

Fig. 1B

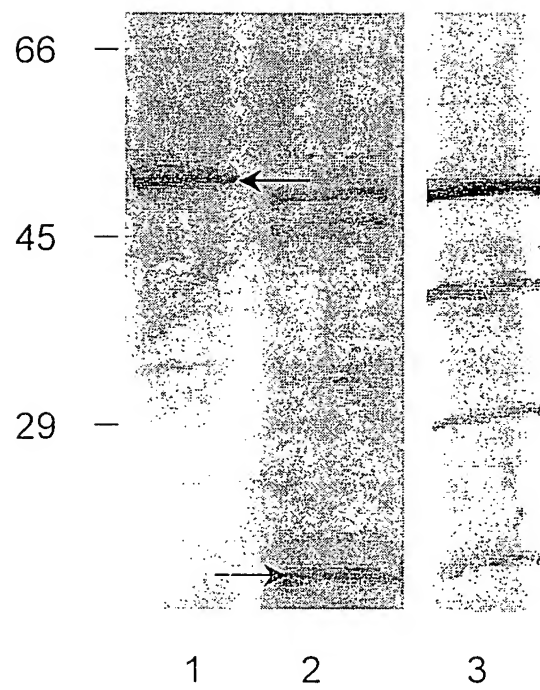


Fig. 2

ECaP28	↓	MNCKKILITLISLMSIPSISFSDTIQDGNMG-GN---- <td>70</td>	70
ECa28SA2	VFTIS....SI.FL.NV.Y.NPVYGNS.-Y-----M...P...I...E.-----K.K.TV.Y...E	70
ECa28SA1		.KY..TFTV...VL.TSFTHF.P.YSPARASTIH-----M.TA...I...-----QSF.KVLV..DQ	69
EChP28		..Y..VF..S....IS.L.GV...PA-GSGIN-----M..A...V...-----RNT.....Q	69
OMP-1B		..Y...FVSS.....SIL.YQ..A.PVTSNDT.INDSREG...V.N.I...RK...E.APINGNTSI.KK.....K	80
OMP-1C	FF....ALP.SFL.G.LL.EPV.DSVS-----M..A...V...-----KNP..ALY...Q	70
OMP-1D		...E.FF....TL..SFL.G..L.PV.D.IS-----M..A...V...-----RNT.....IEQ	70
OMP-1E	FF....V...SFL.G....PV.GD.IS-----V...M..A...M...-----KNP..ALY...Q	70
OMP-1F	FF...T.V...SFL.G....AV.ND.V-----V...Q-----RNT.T.....Q	70
MAP-1	F..ST...VSFL.GV...V..EE.NPV.S-----V...A..M.TA...KM.I..-----D.RD.KA.....K	71
		VR1	
ECaP28		DWDGSPILKNKHAD-FTVPNYSFRYENNPFLGFAGAIGYSMGGPRIEFEIISYEAFDVKSPNINYQNDAH--RYCALSH--	145
ECa28SA2		N.A.DA.SSQSPD.N..IR....K.AS.K....V....I.S....V.M.....NQGN. (SEQ ID NO: 7)	133
ECa28SA1		RLSHNI.NN.DT.KSLK.Q...K.K.....I.NS...L.V.H.I..T.N.GN..L..S.--K.....GS	147
EChP28		N...A.SNSSPN.V...S...K.....D.....L.V...T...NQGN..K.E.-----	145
OMP-1B		-----GDIAQSAN.NRTDPALEFQ..LIS..S.S..A.D....L.AA.QK..A.N.DN.DT.SGDYK.FG..RED	154
OMP-1C		..N.-VSASSHADAD.NNKG...K.....V...T...NQGG..K.....DR--	145
OMP-1D		..RCV.SRTTILS.I.....K...L.S.....D....L.V.....NQGN..K.E.--Y.....	146
OMP-1E		..E.-ISSSSHNDNH.NNKG...K.....V...V...T...NQGN..K.....GQ--	145
OMP-1F	T.S..SPENT.N.....K.....V..L.N....L.M..T...NQGN..K.....K.Y..T.--	146
MAP-1	VKTPSGNTNSI..EKD...K.....V...N.....V...T...RN.GG..K.....M.....	145
		VR2	

Fig. 3A

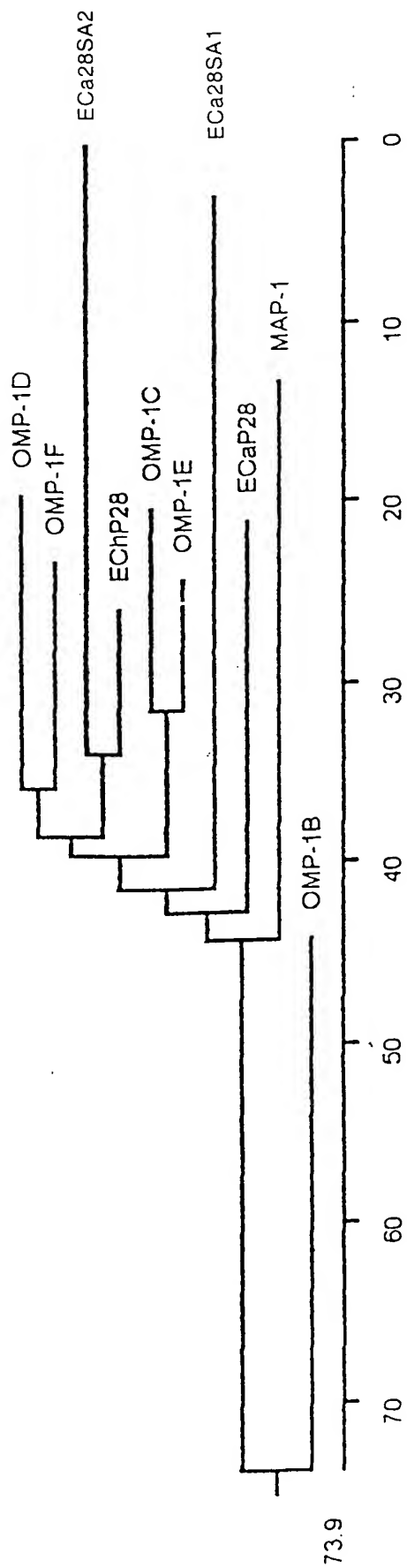


Fig. 4

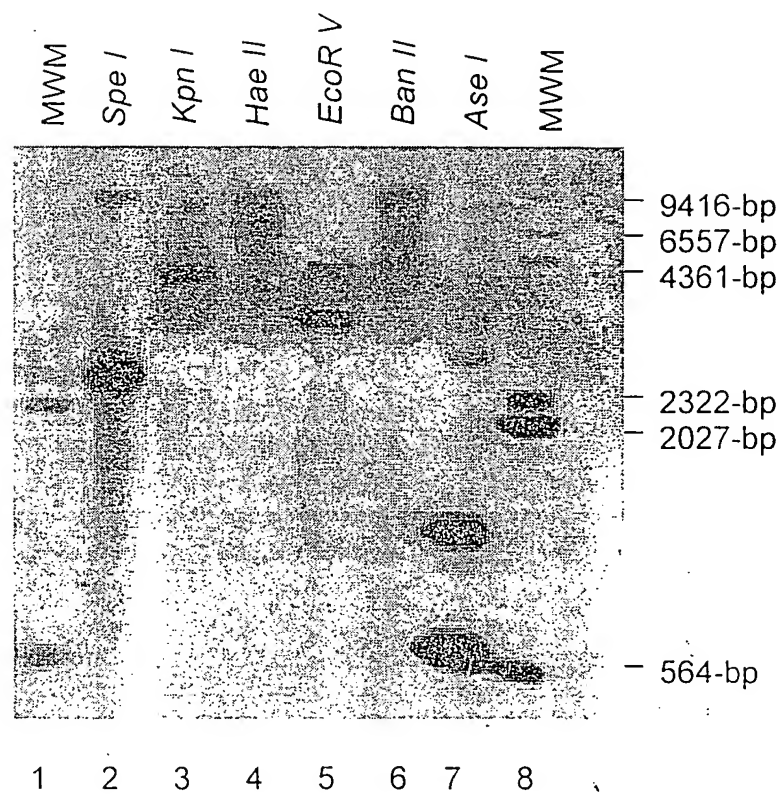
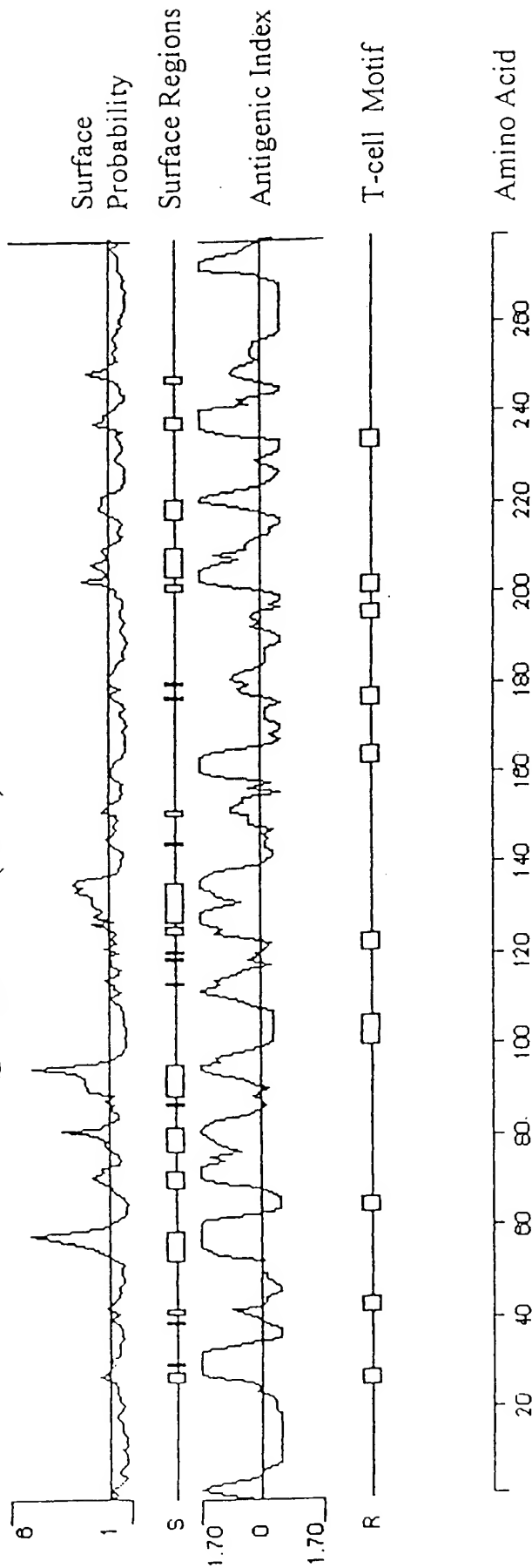


Fig. 5

E. canis P28 (Jake)



E. chaffeensis P28 (Arkansas)

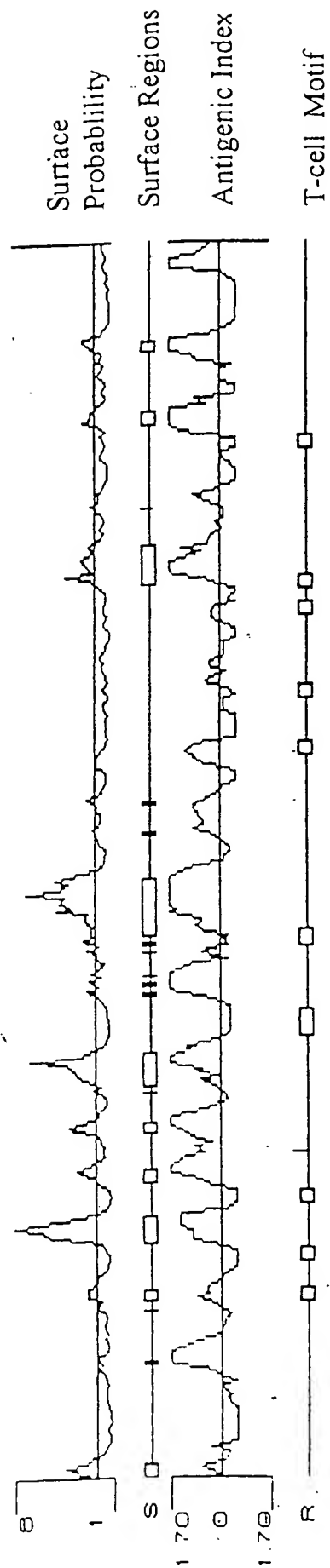


Fig. 6

Eca28SA2

ATGAATTGTAAAAAGTTTTCACAAATAAGTGCATTGATATCATCCATATACTTCCTACCT 60
M N C K K V F T I S A L I S S I Y F L P

AATGTCTCATACTCTAACCCAGTATATGGTAAACAGTATGTATGGTAAATTTTACATATCA 120
N V S Y S N P V Y G N S M Y G N F Y I S

GAAAGTACATGCCAAGTGTTCCTCATTTTGGAAATTTTTCAGCTGAAGAGAGAAAAA 180
G K Y M P S V P H F G I F S A E E K K

AAGACAACTGTAGTATATGGCTTAAAGAAAACTGGGCAGGAGATGCAATATCTAGTCAA 240
K T T V V Y G L K E N W A G D A I S S Q

AGTCCAGATGATAAATTTTACCATTTCGAAATTTACTCATTTCAAGTATGCAAGCAACAAGTTT 300
S P D D N F T I R N Y S F K Y A S N K F

TTAGGGTTTGCAGTAGCTATTGGTTACTCGATAGGCAGTCCAAAGAAATAGAAAGTTGAGATG 360
L G F A V A I G Y S I G S P R I E V E M

TCTTATGAAGCATTTGATGTGAAAAATCCAGGTGATAATTACAAAAACGGTGCTTACAGG 420
S Y E A F D V K N P G D N Y K N G A Y R

TATTGTGCTTTATCTCATCAAGATGATGCGGATGATGACATGACTAGTGCAACTGACAAA 480
Y C A L S H Q D D A D D D M T S A T D K

TTTGTATATTTAATGAAGGATTACTTAACATATCATTTATGACAAAACATATGTTAT 540
F V Y L I N E G L L N I S F M T N I C Y

GAAACAGCAAGCAAAAATATACCTCTCTCTCTTACATATGTGCAGGTATTTGGTACTGAT 600
E T A S K N I P L S P Y I C A G I G T D

TTAATTACATGTTTGAAACTACACATCTCTAAAAATTTCTTATCAAGGAAAGCTAGGGTTG 660
L I H M F E T T H P K I S Y Q G K L G L

Fig. 7A

GCCTACTTCGTAAGTGCAGAGTCTTCGGTTCTCTTTTGGTATATATTTTCATAAAATATA 720
 A Y F V S A E S S V S F G I Y F H K I I
 AATAATAAGTTTAAATAATGTTCCAGCCATGGTACCTATTAACTCAGACGAGATAGTAGGA 780
 N N K F K N V P A M V P I N S D E I V G
 CCACAGTTTGCAACAGTAACATTAAATGTATGCTACTTTGGATTAGAACTTGGATGTAGG 840
 P Q F A T V T L N V C Y F G L E L G C R
 TTCAACTTCTAAATTCGTGGTACACATATCACGAAGCTAAATTTGTTTTTATCTCTGC 900
 F N F * (SEQ ID NO: 4)
 (SEQ ID NO: 3)
 TGTATACAAGAGAAAAATAGTAGTGAAAAATTACCTAAACAATATGACAGTACAAAGTTTAC 960
 CAAGCTTATTCTCAGAAAACTTCTTGTGCTTTTATCTCTTACAAATGAAATGTACACTT 1020
 AGCTTCACACTAGTAGTGTTTATCAATGCTTTGTTTATTAATACTCTACATAATAT 1080
 GTTAAATTTTCTTACAAAACTCACTAGTAATTTATATACTAGAAATATATTTCTGACTTGT 1140
 (SEQ ID NO: 31)
ECa28SA3
 ATTTGCTTTTATACTTCCACTATTGTTAAATTTATTTTCACTATTTTAGGTGTAATATGAAT 1200
 M N
 TGCAAAAAAATTCTTTATAACAACACTGCATTAAATGTCATTAAATGTACTATGCTCCAAGCATA 1260
 C K K I L I T T A L M S L M Y Y A P S I
 TCTTTTCTGATACTATACAAGACGATAACACTGGTAGCTTCTACATCAGTGGAAAAATAT 1320
 S F S D T I Q D D N T G S F Y I S G K Y
 GTACCAAGTGTTTCACATTTTGGTGTTTTTCTCAGCTAAAGAAAGAAACTCAACTGTT 1380
 V P S V S H F G V F S A K E E R N S T V
 GGAGTTTTTGGATTAAACATGATTGGAATGGAGGTACAATATCTAACTCTTCTCCAGAA 1440
 G V F G L K H D W N G G T I S N S S P E

Fig. 7B

AATATATTACAGTTCAAAATTAATTCGTTTAAATACGAAAAACAACCCATTCCTTAGGGTTT 1500
 N I F T V Q N Y S F K Y E N N P F L G F
 GCAGGAGCTATTGGTTATTCAATGGGTGGCCCAAGAAATAGAACTTGAAGTTCTGTACGAG 1560
 A G A I G Y S M G G P R I E L E V L Y E
 ACATTGATGTGAAAAATCAGAAACAATAATTATAAGAACGGCGCACACAGATACTGTGCT 1620
 T F D V K N Q N N N Y K N G A H R Y C A
 TTATCTCATCAGTTCAGCAACAAGCATGTCCCTCCGCAAGTAACAAAATTGTGTTTCTTA 1680
 L S H S S A T S M S S A S N K F V F L
 AAAAAATGAAGGGTTAATTGACTTATCATTTATGATAAAATGCATGCTATGACATAATAATT 1740
 K N E G L I D L S F M I N A C Y D I I I
 GAAGGAATGCCTTTTTCACCTTATATTGTGTCAGGTGTTGGTACTGATGTTGTTTCCATG 1800
 E G M P F S P Y I C A G V G T D V V S M
 TTTGAAGCTATAAAATCCTAAAAATTCTTACCAAGGAAAACTAGGATTAGGTTATAGTATA 1860
 F E A I N P K I S Y Q G K L G L G Y S I
 AGTTCAGAAAGCCTCTGTTTTTATCGGTGGACACTTTCACAGAGTCATAGGTAATGAATTT 1920
 S S E A S V F I G G H F H R V I G N E F
 AGAGACATCCCTGCTATGGTTCCTAGTGGATCAAATCTCCAGAAAACCAATTTGCAATA 1980
 R D I P A M V P S G S N L P E N Q F A I
 (SEQ ID NO: 5)
 GTAACACTAAATGTGTGTCACCTTTGGCATAGAACTTGGAGGAAGATTTAACCTCTGA 2031
 V T L N V C H F G I E L G G R F N F *
 (SEQ ID NO: 6)

Fig. 7C

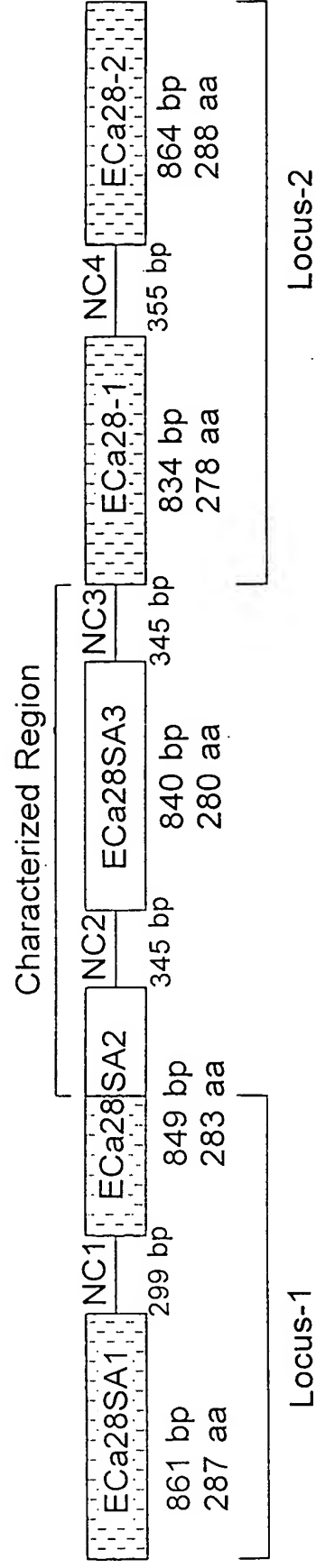


Fig. 8

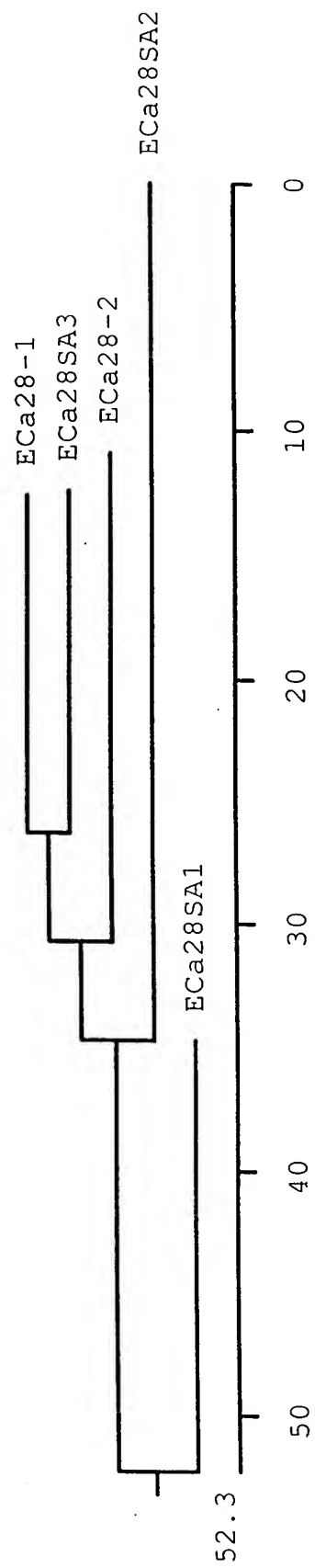


Fig. 9

1	TAATACTTCTATTGT-ACATGTTAAAAATAGTACTAGTTTGCTTCTGTGGTT--TATAAACGCAAGAGAGAA--	28nc1
1	...TTTCGTGG.A-C...A.C.CG.-GC.AA.T.G.TT.T.A.CTC.GC.G.T..AAG...A.A..TA	28nc2
1	.G..TT.AT.G...CC...A.....GA.CTA.AC...T.T.A.TA..GC..C.T..AA..A.A...AA	28nc3
1	...TT.AT.G...CC...A.....GA.CTA.AC...T.T.AWTA..GC..C.T..AA..A.A-...AA	28nc4
70	ATAGT-----TAGTAATAAAATTAGAAAG-----TTAAA--TATT---AGAAAAGT-CA	28nc1
72	G...G--AAAATTACC..AC...TGAC..T.CAAGTTTACC..GCT...CTC.C...C.T.T	28nc2
75GGCAAAAGAATG...C....GAGG.GGG.GGGGAC...TT..CCTTC--T.TTC.T.T	28nc3
74GGCAAAAGAATG...C....GAGG.GGG.GGGGACC...TT..CTTC--T.TGC.T.C	28nc4
112	TATGTTTTTTCATTGTCAATTGAT-ACTCAACTA----AAAGTAGTAT-----AAATGT-----	28nc1
136	.G...C...T..CTCT--T.CA.-G.A.-GTAC.-CT...CT.CACTACTGTAG.G...GTTTATCAATGC	28nc2
139	A..A..C..T---ACT.....T....A..GCAC..CTC.A.GCTTCCA-GG-A...A.GT-TTCTAATAT	28nc3
138	C.A.....TCYC.CT...T.G...T.AC.ACAG..G...A...CCTCACGG-A...CT.ATCTTCAAAATAT	28nc4
159	--TACTTATTAAATAAT-TTTACGTAGTATATTAAATTTCCCTTACAAAAGCCACTAGTATTTTATA	28nc1
205	TT.GT.....-C.C..A..A..G.....TT.....CT.....A.....	28nc2
202	TT..T.....CC..CC..TA..A.....T.....AT.T...A.G.....	28nc3
211	TT..T.....CC..C-..TA..A.....T.....AT.....	28nc4
222	CTAAAAGC-TATACTTTGGCTTGTATTTAATTGTATTTTACTACTGTAAATTACTT-TCACTGTT---TCT	28nc1
269	..T.G.ATA...T.C..A.....GC..A..C.CC...T.....T.....A....TA	28nc2
268	..T..TATA...T.C.....C....C.C.CC...T.....T.....A....TA	28nc3
276	.C-...ATA...T.C..A...CT...CT..C..C.C.C...T.T.....T.G....A..AGG.TA	28nc4
-35		
292	GGTGTAAT 28nc1 (SEQ ID NO: 30)	
338- 28nc2 (SEQ ID NO: 31)	
339- 28nc3 (SEQ ID NO: 32)	
339	TA-A...-W 28nc4 (SEQ ID NO: 33)	
RBS		
-10		

Fig. 10

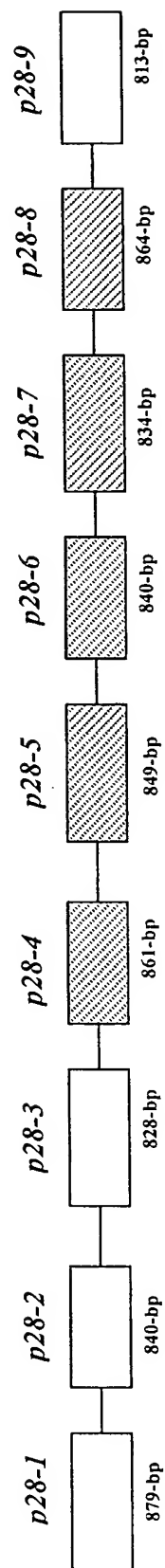


Fig. 11

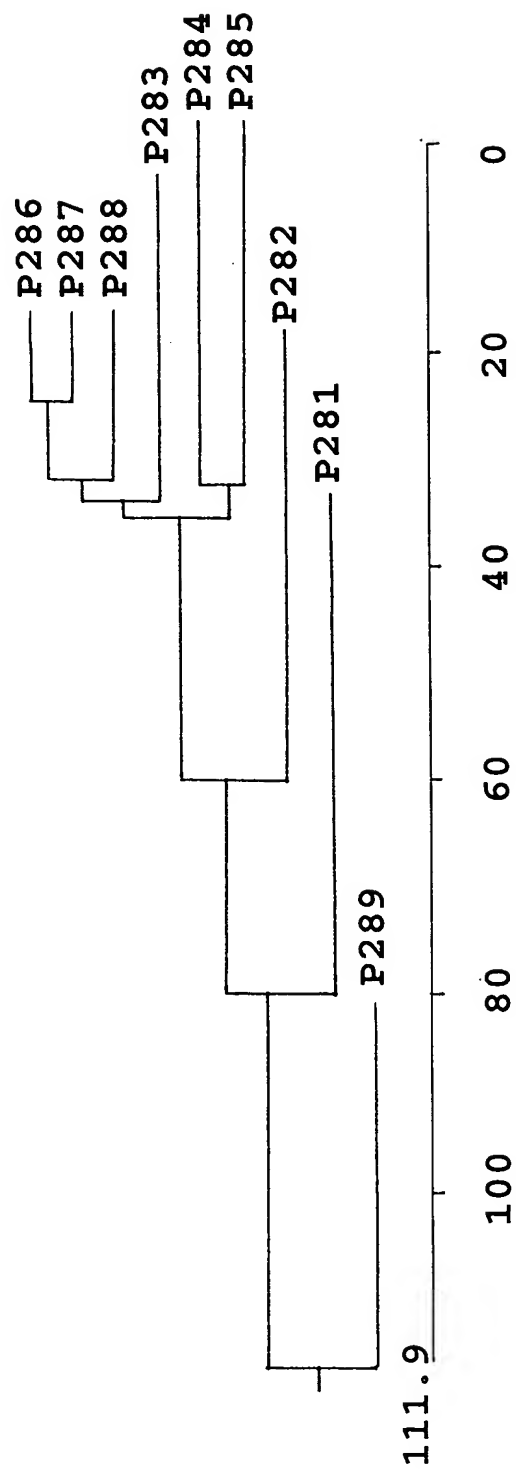


Fig. 12

ATGAATAATAAACTCAAATTTACTATAATAAACACAGTATTAGTATGCTTATTGTCATTA 60
 M N N K L K F T I I N T V L V C L L S L

CCTAATATATCTTCCTCAAAGGCCATAACAATAACGCTAAAAAGTACTACGGATTATAT 120
 P N I S S S K A I N N N A K K Y Y G L Y

ATCAGTGGACAATATAAACCCAGTGTTTCTGTTTTTCAGTAATTTTTCAGTTAAAGAAACC 180
 I S G Q Y K P S V S V F S N F S V K E T

AATGTCATAACTAAAAACCTTATAGCTTTAAAAAAGATGTTGACTCTATTGAAACCAAG 240
 N V I T K N L I A L K K D V D S I E T K

ACTGATGCCAGTGTAGGTATTAGTAACCCATCAAATTTTACTATCCCCTATACAGCTGTA 300
 T D A S V G I S N P S N F T I P Y T A V

TTTCAAGATAATTCTGTCAATTTCAATGGAACCTATTGGTTACACCTTTGCTGAAGGTACA 360
 F Q D N S V N F N G T I G Y T F A E G T

AGAGTTGAAATAGAAGGTTCTTATGAGGAATTTGATGTTAAAAACCCTGGAGGCTATACA 420
 R V E I E G S Y E E F D V K N P G G Y T

CTAAGTGATGCCTATCGCTATTTTGCATTAGCACGTGAAATGAAAGGTAATAGTTTTCATA 480
 L S D A Y R Y F A L A R E M K G N S F T

CCTAAAGAAAAAGTTTCTAATAGTATTTTTCACACTGTAATGAGAAATGATGGATTATCT 540
 P K E K V S N S I F H T V M R N D G L S

ATAATATCTGTTATAGTAAATGTTTGCTACGATTTCTCTTTGAACAATTTGTCAATATCG 600
 I I S V I V N V C Y D F S L N N L S I S

CCTTACATATGTGGAGGAGCAGGGGTAGATGCTATAGAATTCTTCGATGTATTACACATT 660
 P Y I C G G A G V D A I E F F D V L H I

AAGTTTGCATATCAAAGCAAGCTAGGTATTGCTTATTCTCTACCATCTAACATTAGTCTC 720
 K F A Y Q S K L G I A Y S L P S N I S L

TTTGCTAGTTTATATTACCATAAAGTAATGGGCAATCAATTTAAAAATTTAAATGTCCAA 780
 F A S L Y Y H K V M G N Q F K N L N V Q

CATGTTGCTGAACTTGCAAGTATACCTAAAATTACATCCGCAGTTGCTACACTTAATATT 840
 H V A E L A S I P K I T S A V A T L N I

GGTTATTTTGGAGGTGAAATTGGTGCAAGATTGACATTT (SEQ ID No. 39) 879
 G Y F G G E I G A R L T F (SEQ ID NO. 40)

Fig. 13

ATGAATTATAAGAAAATTCTAGTAAGAAGCGCGTTAATCTCATTAATGTCAATCTTACCA 60
 M N Y K K I L V R S A L I S L M S I L P
 TATCAGTCTTTTGCAGATCCTGTAGGTTCAAGAACTAATGATAACAAAGAAGGCTTCTAC 120
 Y Q S F A D P V G S R T N D N K E G F Y
 ATTAGTGCAAAGTACAATCCAAGTATATCACACTTTAGAAAATTCTCTGCTGAAGAACT 180
 I S A K Y N P S I S H F R K F S A E E T
 CCTATTAATGGAACAAATTCTCTCACTAAAAAAGTTTTTCGGACTAAAGAAAGATGGTGAT 240
 P I N G T N S L T K K V F G L K K D G D
 ATAACAAAAAAGACGATTTTACAAGAGTAGCTCCAGGCATTGATTTTCAAATAACTTA 300
 I T K K D D F T R V A P G I D F Q N N L
 ATATCAGGATTTTTCAGGAAGTATTGGTTACTCTATGGACGGACCAAGAATAGAACTTGAA 360
 I S G F S G S I G Y S M D G P R I E L E
 GCTGCATATCAACAATTTAATCCAAAAACACCGATAACAATGATACTGATAATGGTGAA 420
 A A Y Q Q F N P K N T D N N D T D N G E
 TACTATAAACATTTTGCATTATCTCGTAAAGATGCAATGGAAGATCAGCAATATGTAGTA 480
 Y Y K H F A L S R K D A M E D Q Q Y V V
 CTTAAAAATGACGGCATAACTTTTATGTCATTGATGGTTAATACTTGCTATGACATTACA 540
 L K N D G I T F M S L M V N T C Y D I T
 GCTGAAGGAGTATCTTTCGTACCATATGCATGTGCAGGTATAGGAGCAGATCTTATCACT 600
 A E G V S F V P Y A C A G I G A D L I T
 ATTTTAAAGACCTCAATCTAAAATTTGCTTACCAAGGAAAAATAGGTATTAGTTACCCT 660
 I F K D L N L K F A Y Q G K I G I S Y P
 ATCACACCAGAAGTCTCTGCATTTATTGGTGGATACTACCATGGCGTTATTGGTAATAAA 720
 I T P E V S A F I G G Y Y H G V I G N K
 TTTGAGAAGATACCTGTAATAACTCCTGTAGTATTAAATGATGCTCCTCAAACCACATCT 780
 F E K I P V I T P V V L N D A P Q T T S
 GCTTCAGTAACTCTTGACGTTGGATACTTTGGCGGAGAAATTGGAATGAGGTTACCTTC 840
 A S V T L D V G Y F G G E I G M R F T F
 (SEQ ID No. 41)
 (SEQ ID No. 42)

Fig. 14